

FIG 1



FIG. 2

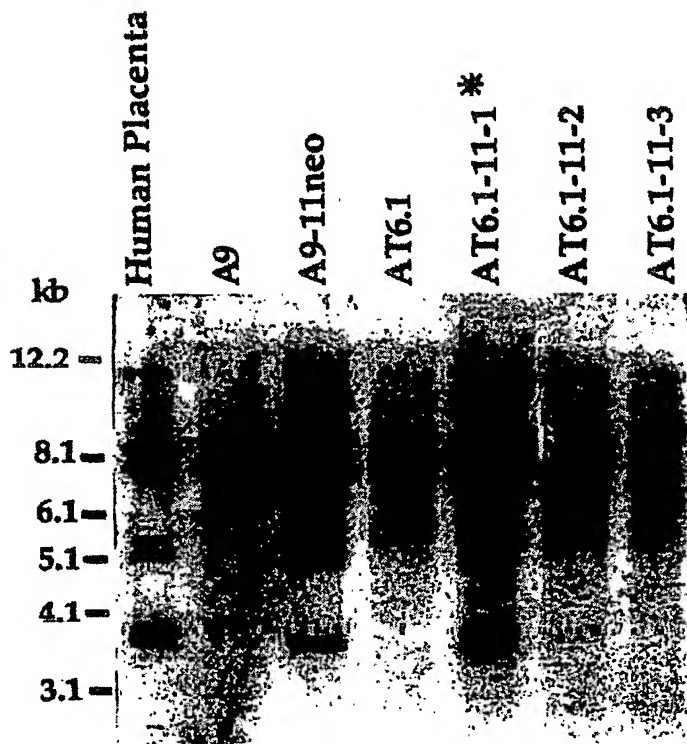


FIG. 3

1 CCGACTGAGGCACGAGCGGGTGACGCTGGGCCTGCAGCGCGGAGCAGAAAGCAGAACCCG
61 CAGAGTCCTCCCTGCTGTGTGGACGACACGTGGGCACAGGCAGAAGTGGGCCCTGTG
121 ACCAGCTGCACTGGTTCGTGGAAGGAAGCTCCAGGACTGGCGGGATGGGCTCAGCCTGT
1 M G S A C
181 ATCAAAGTCACCAAATACTTTCTCTTCTTCAACTTGATCTTCTTTATCCTGGGCGCA
6 I K V T K Y F L F L F N L I F F I L G A
241 GTGATCCTGGGCTTCGGGGTGTGGATCCTGGCCGACAAGAGCAGTTTCATCTCTGTCTG
26 V I L G F G V W I L A D K S S F I S V L
301 CAAACCTCCTCCAGCTCGCTTAGGATGGGGGCTATGTCTTCATCGGCGTGGGGGCGAGTC
46 Q T S S S S L R M G A Y V F I G V G A V
361 ACTATGCTCATGGGCTTCTGGGCTGCATCGGCGCCGTCAACGAGGTCCGCTGCTGCTG
66 T M L M G F L G C I G A V N E V R C L L
421 GGGCTGTACTTTGCTTTCTGCTCCTGATCCTCATTGCCAGGTGACGGCCGGGGCCCTC
86 G L Y F A F L L L I L I A Q V T A G A L
481 TTCTACTTCAACATGGGCAAGCTGAAGCAGGAGATGGGCGGCATCGTGACTGAGCTCATT
106 F Y F N M G K L K Q E M G G I V T E L I
541 CGAGACTACAACAGCAGTCGCGAGGACAGCCTGCAGGATGCCTGGGACTACGTGCAGGCT
126 R D Y N S S R E D S L Q D A W D Y V Q A
601 CAGGTGAAGTGCTGCGGCTGGGTGAGCTTCTACAAGTGAAGGAGACAACGCTGAGCTCATG
146 Q V K C C G W V S F Y N W T D N A E L M
661 AATCGCCCTGAGGTACCTACCCCTGTTCCTGCGAAGTCAAGGGGGAAGAGGACAACAGC
166 N R P E V T Y P C S C E V K G E E D N S
721 CTTTCTGTGAGGAAGGGCTTCTGCGAGGCCCCGGCAACAGGACCCAGAGTGGCAACCAC
186 L S V R K G F C E A P G N R T Q S G N H
781 CCTGAGGACTGGCCTGTGTACCAGGAGGGCTGCATGGAGAAGGTGCAGGCGTGGCTGCAG
206 P E D W P V Y Q E G C M E K V Q A W L Q
841 GAGAACCTGGGCATCATCCTCGGCGTGGGCGTGGGTGTGGCCATCATCGAGCTCCTGGGG
226 E N L G I I L G V G V G V A I I E L L G
901 ATGGTCCTGTCCATCTGCTTGTGCCGGCACGTCCATTCCGAAGACTACAGCAAGGTCCCC
246 M V L S I C L C R H V H S E D Y S K V P
961 AAGTACTGAGGCAGCTGCTATCCCCATCTCCCTGCCTGGCCCCCAACCTCAGGGCTCCCA
266 K Y *
1021 GGGGTCTCCCTGGCTCCCTCCTCCAGGCCTGCCTCCCACTTCACTGCGAAGACCCCTCTTG
1081 CCCACCCTGACTGAAAGTAGGGGGCTTTCTGGGGCCTAGCGATCTCTCCTGGCCTATCCG
1141 CTGCCAGCCTTGAGCCCTGGCTGTTCTGTGGTTCTCTGCTCACC GCCCATCAGGGTTCT
1201 CTTATCAACTCAGAGAAAAATGCTCCCCACAGCGTCCCTGGCGCAGGTGGGCTGGACTTC
1261 TACCTGCCCTCAAGGGTGTGTATATTGTATAGGGGCAACTGTATGAAAAATTTGGGGAGGA
1321 GGGGGCCGGGCGGGTGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTG
1381 GATCACGAGGTGAGGAGATCGAGACCATCCTGGCTAACATGGTGAAACCCCGTCTCTACT
1441 AAAAATACAAAAAAATTTAGCCGGGCGGGTGGCGGGCACCTGTAGTCCCAGCTACTTG
1501 GGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGCGGAGGTGTCAGTGAGCTGAGATC
1561 GTGCTACTGCACTCCAGCCTGGGGGACAGAAAGAGACTCCGTCTCAAAAAAAAAAAAAA
1621 AAAA

FIG. 4

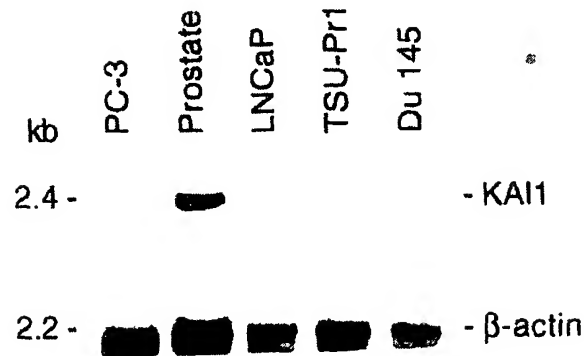


FIG. 5

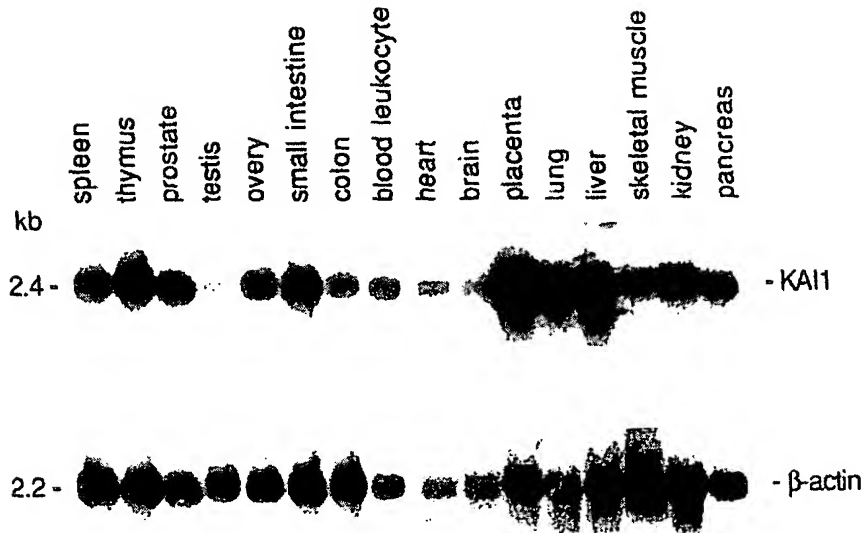


FIG. 6

